
Genes VII

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Figure 1.6 The double helix maintains a constant width because purines always face pyrimidines in the complementary A-T and G-C base pairs. The sequence in the figure is
 T-A
 C-G
 A-T
 G-C

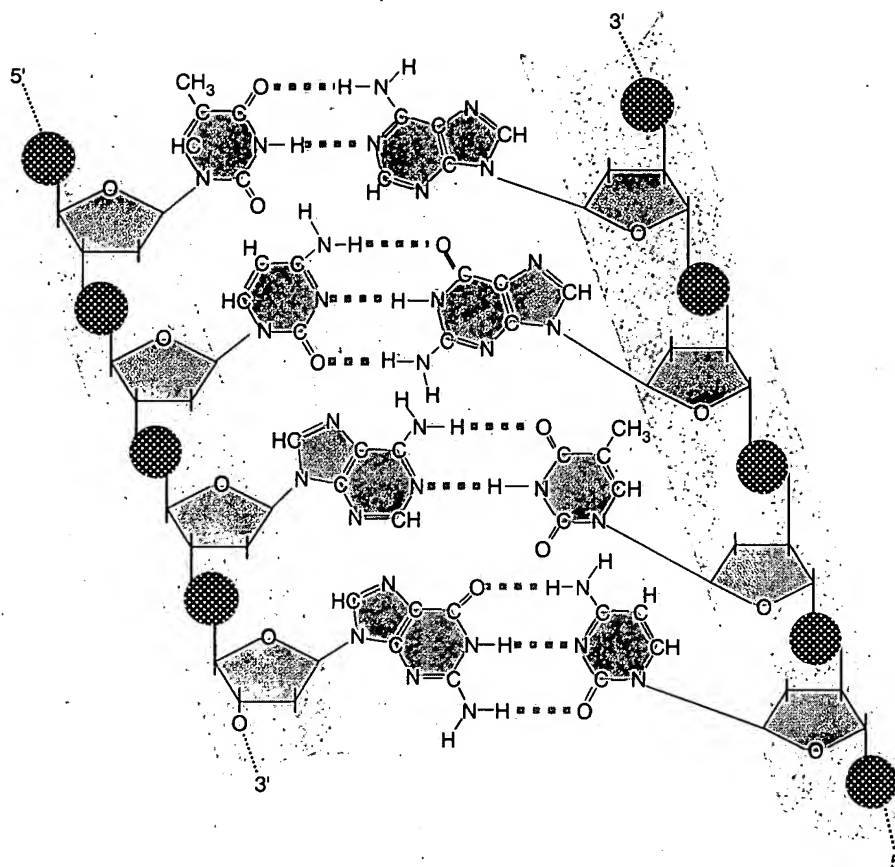
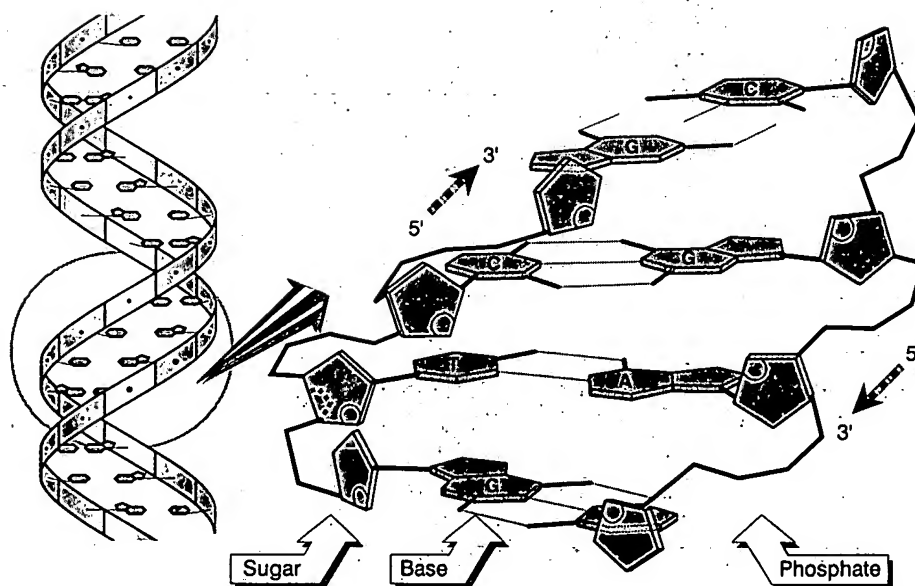


Figure 1.7 Flat base pairs lie perpendicular to the sugar-phosphate backbone.



■ Irrespective of the actual amounts of each base, the proportion of G is always the same as the proportion of C in DNA, and the proportion of A is always the same as that of T. So the composition of any DNA can be described by the proportion of its bases, that is G + C. This ranges from 26% to 74% for different species.

Watson and Crick proposed that the two polynucleotide chains in the double helix associate by *hydrogen bonding between the nitrogenous bases*. G can hydrogen bond specifically only with C, while A can bond specifically only with T. These reactions are described as **base pairing**, and the paired bases (G with C, or A with T) are said to be **complementary**.

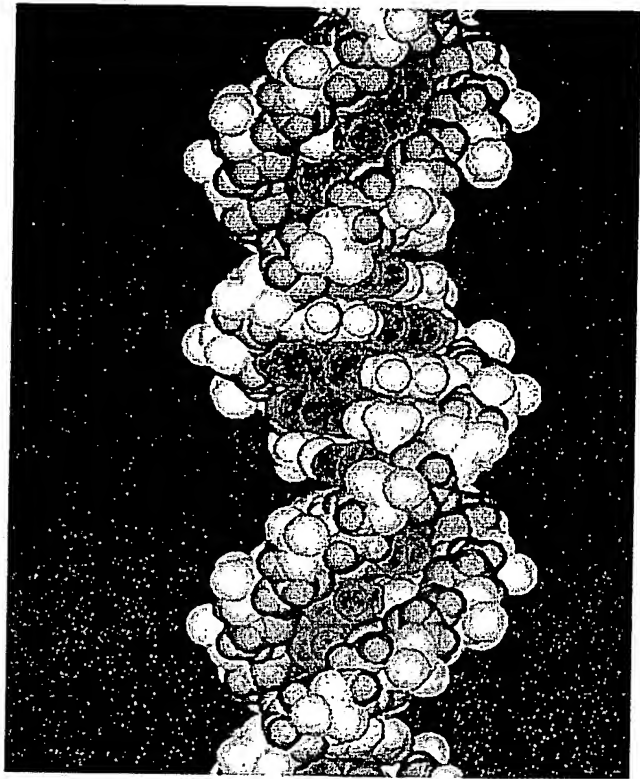
The model requires the two polynucleotide chains to run in opposite directions (**antiparallel**), as illustrated in Figure 1.6. Looking along the helix, therefore, one strand runs in the 5'→3' direction, while its partner runs 3'→5'.

The sugar-phosphate backbone is on the outside and carries negative charges on the phosphate groups. When DNA is in solution *in vitro*, the charges are neutralized by the binding of metal ions, typically by Na^+ . In the natural state *in vivo*, positively charged proteins provide some of the neutralizing force. These proteins play an important role in determining the organization of DNA in the cell.

The bases lie on the inside. They are flat structures, lying in pairs perpendicular to the axis of the helix. Consider the double helix in terms of a spiral staircase: the base pairs form the treads, as illustrated schematically in Figure 1.7. Proceeding along the helix, bases are stacked above one another, in a sense like a pile of plates.

Each base pair is rotated $\sim 36^\circ$ around the axis of the helix relative to the next base pair. So ~ 10 base pairs make a complete turn of 360° . The twisting of the two

Figure 1.8 The two strands of DNA form a double helix.



strands around one another forms a double helix with a **narrow groove** ($\sim 12 \text{ \AA}$ across) and a **wide groove** ($\sim 22 \text{ \AA}$ across), as can be seen from the scale model in Figure 1.8. The double helix is **right-handed**; the turns run clockwise looking along the helical axis. These features represent the accepted model for what is known as the **B-form** of DNA.

DNA replication is semiconservative

IT is crucial that the genetic material is reproduced accurately. Because the two polynucleotide strands are joined only by hydrogen bonds, they are able to separate without requiring breakage of covalent bonds. The specificity of base pairing suggests that each of the sep-

arated **parental strands** could act as a **template** for the synthesis of a complementary **daughter strand**, as depicted in Figure 1.9. The principle is that a new daughter strand is assembled on each parental strand. The sequence of the daughter strand is dictated by the